

SEQUENCE LISTINGS

## (2) INFORMATION FOR SEQ ID NO: 1:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2623 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Rattus norvegicus

(B) TISSUE TYPE: Dorsal root ganglion

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 292..1909

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

spasic Length: 2622

1 AGTGACAGCT GTGCGGGTGC TGATAAGGGA AGCCACAAGG AGACGATCGA

51 GGAGAGAGAC AAGCGGCAGC AGAGGCAGCA GCGACAGATG CAGCGCCGGG

101 GCTGCGGAGC TGCTGGAGT GGGAGTGACG CCCCCACCTC GGGCCCCAC

151 CCTGTCCCCA TCCTCCTCCT GGTTGCCCTG AGTTTAGAAG AGCAGCCGCT

201 GCCACCACCA CCACTCCGGA GGGCACCAGG GCTGCTGTCC AGGGAAGGAC

251 AGTAGCAGTG AGGCTCTGGC CAGTCCCAGC AGCCGGGAC AGATGCCGAT

301 CGAGATTGTG TGCAAAATCA AATTGCTGA GGAGGATGCA AAACCCAAGG

351 AGAAGGAGGC AGGGGATGAG CAGAGCCTCC TGGGGGCTGC TCAGGGGCCA

401 GCAGCCCCCTC GGGACCTGGC TACCTTGCC AGCACCAGTA CTCTGCATGG

2

451 GCTGGGCCGG GCCTGTGGCC CAGGCCCCA TGGACTGCGC AGAACCTGT  
 501 GGGTACTGGC CCTACTCACC TCACTGGCTG CCTTCCTGTA CCAGGCAGCC  
 551 AGCCTGGCCA GGGGCTACCT GACCCGGCCT CACCTGGTAG CCATGGACCC  
 601 TGCTGCCCA GCCCCAGTGG CGGGCTTCC GGCTGTCAAC CTCTGCAACA  
 651 TCAACCGCTT CCGGCATTG GCACTCAGCG ATGCTGATAT CTTCCACCTG  
 701 GCCAATCTGA CAGGGCTGCC CCCCAAAGAC CGGGATGGC ACCGTGCAGC  
 751 TGGCCTTCGC TACCCAGAGC CTGACATGGT AGACATCCTC AACCGCACTG  
 801 GCCACCAGCT TGCTCACATG CTCAAGAGCT GCAACTTCAG TGGGCACCA  
 851 TGCTCCGCCA GCAACTTCCTC TGTGGTCTAT ACTCGCTATG GAAAGTGTAA  
 901 CACCTTCAAT GCAGATCCTC AGAGTTCACT GCCCAGCAGG GCAGGCGGA  
 951 TGGGTAGTGG CCTGGAGATC ATGCTAGACA TCCAGCAGGA GGAATACCTA  
 1001 CCCATATGGA GGGAGACAAA TGAGACATCA TTCGAGGCAG GGATCCGGGT  
 1051 GCAGATCCAC AGCCAGGAGG AGCCTCCCTA CATCCACCAG CTGGGGTTCG  
 1101 GTGTGTCCCC AGGCTTCCAG ACTTTGTGT CCTGCCAGGA ACAGCGGCTA  
 1151 ACTTATCTGC CCCAGCCTTG GGGCAACTGC CGGGCGGAAA GCAAGCTCAG  
 1201 GGAGCCTGAG CTTCAGGGCT ACTCAGCCTA TAGTGTGTCT GCCTGCCGAC  
 1251 TGCCTGTGA GAAGGAGGCC GTGCTTCAGC GCTGCCACTG CGGGATGGTG  
 1301 CACATGCCAG GCAATGAGAC CATCTGCCCG CCAAATATCT ACATTGAATG  
 1351 TGCCGACCAC ACAGTGGACT CCCTGGGTGG GGGCTCTGAG GGCCCATGCT

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1st  
 C6  
 Cont

1401 TCTGCCCTAC ACCCTGCAAC CTGACTCGTT ACGGCAAAGA GATCTCCATG  
 1451 GTCAAGATCC CCAACAGGGG CTCTGCCAGG TACCTGGCGA CGAAGTACAA  
 5 1501 CCGCAATGAG ACCTACATAA GGGAAAAC TTGGTCTG GATGTCTTCT  
 1551 TTGAGGCCCT AACCTCTGAA GCCATGGAAC AGCGAGCTGC CTATGGTCTG  
 1601 TCAGCCTTGC TGGGGGACCT TGGGGGACAG ATGGGCCTGT TCATTGGGC  
 10 1651 TAGCATCCTC ACCTTGCTGG AGATCCTTGA CTACATCTAT GAGGTCTCCT  
 1701 GGGATCGACT CAGAGGGTG TGGCGACGGC CCAAGACCCC ACTTAGGACG  
 15 1751 TCCACTGGGG GCATCTCCAC TTTGGGGCTG CAGGAACTGA AGGAACAGAG  
 1801 TCCCTGTCCA AATCGAGGCC GTGCTGAGGG TGGTGGGGCT AGAACCTGC  
 1851 TTCCCAACCA TCACCACCCC CACGGCCCCC CAGGAAGCCT CTTTGAAAAC  
 20 1901 TTTGCTTGCT AGGATGGTGC TGTGTGGGA AAGTACCCAT GAAACCCAC  
 1951 ACTCTCCTAT TCCTGGACA GAAGGTCTGG GGCAGCCCAG GGCTAAGGG  
 25 2001 AGGGGTGGTG CTCACTGAAA GGCCAGGACT AGGGTCTGC TCTCCCTGAC  
 2051 CTAGGCTCAG CTGCCTTGCA CAAGAACCT TCTTGTCAT ACTCCCTGCT  
 2101 CCCAGGCAGG TGTCCAGGAA GGGCTAGAGA CCGGACTANG AGGCCCTGA  
 30 2151 GGAGGGGAGG GATGAAGAGA GGGAGGAAGG CGGAACCATG GTAGAGCCCC  
 2201 TCNGTACATT TGTATATATT TAGGGACTGG GTGGGGTGG GACACAGACA  
 2251 TANAAGGTTT GGGCTGCAGG GGAGGGTGAC ACAGGATAGT CAGGGTCCCA  
 35 2301 ACCCTAATGG CANAANGCAA CTCCTGGGA CCTAGGCATG TTGGGCTGGT

full  
 C6  
 cont

2351 TCTACTTCCC TCTTTCCAGG CCCAGCTCCC TCTTGGCATG GGGAGTGGGT  
2401 GGCCCATCAG GCCTGGCCA GCTCCCANTT CCCCCTGTAC CAGCCCCACC  
5 2451 ACAAGTTCCC TTCGTGGGA GTGGGTGGAA ANACCTTCAG GACCTTGGCT  
2501 AAGCCTTATGG GGAGANGGAG TGGCCTTCTC ANGCCTTGCT CCCTANAGAC  
2551 TGGTTTTATA AANTGCTGGT GAACTTGGGA ATCNAGAGAC CCCNAGAAAA  
10 2601 AAAAAAAA AAAAAAAA AA

## 15 (2) INFORMATION FOR SEQ ID NO: 2:

20 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 539 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear  
  
(ii) MOLECULE TYPE: protein  
(xi) SEQUENCE DESCRIPTION: SPASIC protein

25 *Sub C6 Cont* 1 MPIEIVCKIK FAEEDAKPKE KAGDEQSLL GAAQGPAAPR DLATFASTST  
51 51 LHGLGRACGP GPHGLRRTLW VLALLTSLAA FLYQAASLAR GYLTRPHLVA  
101 101 MDPAAPAPVA GFPAVTLCNI NRFRHSALSD ADIFHLANLT GLPPKDRDGH  
151 151 RAAGLRYPEP DMVDILNRTG HQLADMLKSC NFSGHHCAS NFSVVYTRYG  
201 201 KCYTFNADPQ SSLPSRAGGM GSGLEIMLDI QQEYLPIWR ETNETSFEAG  
251 251 IRVQIHSQEE PPYIHQLGFG VSPGFQTFVS CQEQLTYLP QPWGNRAES  
301 301 KLREPELQGY SAYSVSACRL RCEKEAVLQR CHCRMVHMPG NETICPPNIY

351 IECADHTLDS LGGGSEGPCF CPTPCNLTRY GKEISMVKIP NRGSARYLAR

401 KYNRNETYIR ENFLVLDVFF EALTSEAMEQ RAAYGLSALL GDLGGQMGLF

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451 IGASILTLLE ILDYIYEVSW DRLKRVWRRP KTPLRTSTGG ISTLGLQELK

501 EQSPCNRGR AEGGGASNLL PNHHHHPHGPP GSLFENFAC

10 (2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 526 amino acids

(B) TYPE: Protein

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(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: ASIC protein

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SEQUENCE DESCRIPTION: SEQ ID NO: 3:

1 MELKTEEEEV GGVQPVSIQA FASSSTLHGL AHIFSYERLS LKRALWALCF

51 LGSLAVLLCV CTERVQYYFC YHHVTKLDEV AASQLTFPAV TLCNLNEFRF

25

101 SQVSKNDLYH AGELLALLNN RYEIPDTQMA DEKQLEILQD KANFRSKPK

151 PFNMREFYDR AGHDIRDMLL SCHFRGEACS AEDFKVVFTR YGKCYTFNSG

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201 QDGRPRLKTM KGGTGNGLEI MLDIQQDEYL PVWGETDETS FEAGIKVQIH

251 SQDEPPFIDQ LGFGVAPGFQ TFVSCQEQLR IYLPSPWGTC NAVTMDSDF

35

301 DSYSITACRI DCETRYLVEN CNCRMVHMPG DAPYCTPEQY KECADPALDF

351 LVEKDQEYCV CEMPCNLTRY GKELSMVKIP SKASAKYLAK KFNKSEQYIG

6

401 ENILVLDIFF EVLNYETIEQ KKAYEIAGLL GDIGGQMGLF IGASILTVLE  
451 LFDYAYEVIK HRLCRRGKQ KEAKRSSADK GVALSLDDVK RHNPCESLRG  
5 501 HPAGMTYAAN ILPHHPARGT FEDFTC

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(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Rattus norvegicus
- (F) TISSUE TYPE: Neurons

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

TAGCAGTGAGGCTCTGGCGAGTCCCA

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*Sub Cle Cmt*  
*25*  
*30*  
*35*

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Rattus norvegicus
- (F) TISSUE TYPE: Dorsal root ganglion

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

CCAGACCTTCTGTCCCAGGAATAGG

5 (2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Rattus norvegicus
- (F) TISSUE TYPE: Dorsal root ganglion

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

20 GACCTGGCTACCTTGCCAGCACCA

25 (2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Rattus norvegicus
- (F) TISSUE TYPE: neurons

30 35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

Substituted  
Sequence  
Sheet  
Rule 26  
Sheet 1 of 1

Sub  
C6  
Gene

ATATGGGTAGGTATTCCTCCTGCTG

2) INFORMATION FOR SEQ ID NO: 8:

5

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Rattus norvegicus*
- (F) TISSUE TYPE: neurons

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

C/AGI, TAT/C, GG/CT, AAA/G, GAA/G, T/C/ATI, TCI, ATG

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2) INFORMATION FOR SEQ ID NO: 9:

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Rattus norvegicus*
- (F) TISSUE TYPE: neurons

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35  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

IC/TT/A, IGC, ICC, IAT, A/GAA, IAG/A, ICC